REMARKS

The Examiner objected to claims 39-40, 42-43, 51-54, 85-86, 88, and 97-100 because of a grammatical informality.

The Examiner stated that the recitation "wherein a plurality of relevance scores are calculated" should be replaced by the recitation "wherein a plurality of relevance scores is calculated". Claims 54 and 100 have been amended to cure the defect.

The Examiner rejected claims 1-56, 80-90, and 92-101 under 35 U.S.C. 101 as being directed to non-statutory subject matter.

The Examiner stated that the claimed invention did not physically transform an article or physical object to a different state or thing (a physical transformation), or otherwise produce a concrete, tangible, and useful result. The Examiner admits that in the instant case the recitation "displaying the gene or protein related data" "does provide a tangible result that is useful to one skilled in the art and thus provides a practical application" but maintains that the claims "must also meet the machine-or-transformation test in order to be eligible under 35 USC 101 as statutory subject matter (In re Bilski, 545 F.3d 943, 88 USPQ2d 1385 (Federal Circuit, 2008)."

Independent claims 1 and 80 have been amended to make it clear that the claimed invention requires two inputs, arbitrary gene- or protein- related data and chromosome maps, and provides a data-enhanced map as an output. The invention transforms the chromosome maps to data-enhanced chromosome map that is displayed. Hence, the claims relate to transforming maps representing real world quantities. Accordingly, Applicant submits that claims 1-56, 80-90, and 92-101 are directed to statutory subject matter.

The Examiner rejected claims 1-4, 7, 10, 12-37, 40, 55, 56, 80-83, and 86 under 35 U.S.C. 103(a) as being unpatentable over Partridge et al. [International Journal of Cancer, volume 83, 1999, pages 318-325] in view of Reeves [genome, 2001, volume 44, pages 439-443]. Applicant submits that as currently amended, claims 1-4, 7, 10, 12-37,

40, 55, 56, 80-83, and 86 are not obvious in view of the cited prior art

The Examiner states that Partridge teaches all the limitations of independent claims 1 and 80 except for the computer/computer display limitations. The Examiner looks to Reeves for the missing teachings. The Examiner maintains that it would have been obvious to modify the chromosomal ordering maps and matrices of Partridge et al. by use of the computation importation and display of Reeves because "automation facilitates the analysis of chromosomes [see abstract of Reeves et al.]".

Claims 1 and 80 have been amended to make it clear that the gene- or protein- related data that are imported and then displayed in adjacent positions on a chromosome map where the data identifiers match the predetermined chromosome map identifiers include data **other than markers or identifiers** specifying genetic loci of that gene- or protein-related data on the chromosome maps. Partridge teaches the importation of "map positions of markers" from the Genome Data base (page 319, first column) but does not teach the importation of other gene- or protein- related data. Moreover, the chromosome maps shown by Partridge (Figures 1-5) show only markers and identifiers adjacent chromosome maps. Reeves does not provide the missing teachings.

Reeves teaches a system that displays images of chromosomes and allows the user to make measurements of distances between points on the chromosomes shown in the pictures. The measurements are then collected in an excel spreadsheet. The images are not even chromosome maps. The Examiner has not pointed to any teaching in either of the references or the art as to how one would modify Partridge to obtain a system that satisfies the limitations of the claims in question absent the specification and claims of the present application, and such hindsight reconstruction cannot be used to construct a rejection under 35 U.S.C. 103. Accordingly, Applicant submits that as currently amended, claims 1, 80 and the claims dependent therefrom are not obvious in view of the cited prior art.

Claim 80 additionally requires that the gene- or protein- related data that are imported and then displayed adjacent identifier-matched positions on a chromosome map include a matrix of at least one microarray of gene expression data. The only matrices taught by Partridge are those shown in Figure 2, which present the results of the allelo-typing

experiments carried out by Partridge. First, these matrices are not imported as an input, but are produced as an output. Second, these matrices are not displayed adjacent positions on a chromosome map. In addition, these matrices contain gene-typing data, not gene expression data.

Claim 80 also requires that the matrix be divided into two smaller matrices with a first matrix containing the columns associated with normal experiments and a second matrix containing the columns associated with abnormal experiments. The Examiner points to the top set of matrices in Figure 2 of Partridge as the recited second matrix and the bottom matrix as the recited first matrix. In both the claim and Partridge, the columns correspond to experiments. However, in Partridge, the two matrices do not result from a division according to columns associated with normal and abnormal experiments respectively. At most, they result from a division according to rows (markers) associated with normal and abnormal chromosomal loci. Accordingly, there are additional grounds for allowing claim 80 and the claims dependent therefrom.

Claim 4 depends from claim 1 and additionally requires that the gene- or protein-related data, which is displayed adjacent identifier-matched positions on a chromosome map, be compressed when it is required to display that gene- or protein-related data in an area in which all of the gene- or protein-related data cannot be discretely displayed. The Examiner points to Figure 1b of Reeves as providing the additional teachings. The cited figure shows a table of data specifying the distances between the points on the images that were marked by the user. First, there is not teaching that this table is to the chromosome images in Figure 1b, no less that it is shown adjacent identifier-matched positions on a chromosome map. Reeves is silent as to the position of the table with respect to the chromosome images shown in Figure 1a. Hence, Reeves does not even teach that the table is adjacent to the picture of the chromosomes. Second, tabulating data is not equivalent to compressing data. The table is the data in question, not a compressed version of the data. Accordingly, there are additional grounds for allowing claim 4.

Claim 7 depends from claim 1 and now explicitly states that the recited focus and context be maintained by displaying at least one chromosome map with overlaid gene- or

protein-related data at a first magnification, and at least one other chromosome map with overlaid gene- or protein-related data at a second magnification, so that both of these maps may be viewed simultaneously, where the first and second magnifications are different. The specification of the current invention provides support for this amendment in paragraphs 0026 and 0144. Neither Partridge nor Reeves teaches the display of maps at different levels of magnification so that they may be viewed simultaneously. Accordingly, there are additional grounds for allowing claim 7 and the claims dependent therefrom.

Claim 10 depends from claim 1 and additionally requires comprising displaying **tooltips** to display additional details relative to a selected portion of the display. The Examiner points to Figure 1b of Reeves as providing the additional teaching. A tooltip is understood in the art to be a brief, descriptive message that appears when a user positions a computer mouse over a particular item shown on the display, the message having particular relevance to that item. Tooltip 544 shown in Figure 7B and discussed in Paragraph 0147 of the specification is one example. Figure 1b of Reeves is simply a table of measurement data, related to several of the features indicated on the chromosomes shown in Figure 1a. There is no teaching that the table appears when a user selects any one item on Figure 1a, nor that the table then contains data relevant to that item. Hence, Figure 1b is not a tooltip. Accordingly, there are additional grounds for allowing claim 10.

Claim 12 depends from claim 1, and has been amended to clarify its additional requirements. The claim now clearly requires that the specific information obtained from an external source, matched with an identifier and displayed relative to the gene- or protein-related data associated with that identifier **comprise data other than markers, identifiers, or a chromosome map.** Neither Partridge nor Reeves teach that such information is obtained, matched and displayed as required. Accordingly, there are additional grounds for allowing claim 12.

Claim 16 depends from claim 1 and further requires that the arbitrary gene- or protein-related data comprise a gene expression matrix or a protein expression matrix, wherein each said row of said matrix contains data values for a particular gene or protein. The Examiner points to the matrices in Figure 2 of Partridge et al. as gene expression matrices.

First, as noted above with respect to claim 80, Applicant submits that the measurement data in the tables of Partridge are not gene expression data but gene typing data. Second, each row in the tables of Partridge contains data for a particular marker, which may span many genes. Accordingly, there are additional grounds for allowing claim 16 and the claims dependent therefrom.

Claim 18 depends from claim 16 and further requires reordering and spatial grouping of the rows of the matrix based on matching the identifiers to the predefined identifiers. The Examiner points to Figure 1 of Partridge as teaching "reorderings of spatial groups" and to the matrices of Figure 2 of Partridge as teaching the other additional limitations of the claim. First, Applicant submits that reordering spatial groups is not the same as reordering AND spatially grouping rows. Second, there is no teaching that the rows in the matrices of Partridge are ever reordered. Accordingly, there are additional grounds for allowing claim 18.

Claim 20 depends from Claim 1 and further requires statistically assessing co-location values and displaying assessed co-location statistical significance along side said arbitrary gene-related data. The Examiner points to Figure 2 of Partridge as providing this teaching. The data shown along side the matrix in Figure 2 of Partridge is not the statistical significance of any of the values shown. Accordingly, there are additional grounds for allowing Claim 20.

Claim 22 depends from claim 1 through claim 21 and additionally requires that annotations be displayed alongside the display of the arbitrary gene- or protein-related data. The Examiner points to Figure 2 of Partridge as providing this teaching, identifying the allelic imbalance, retention of heterozygosity, and microsatellite instability as the annotations. Applicant submits that an annotation is an addition made to pre-existing written material, to offer relevant additional explanation or qualification. The allelic imbalance and other data to which the Examiner points are the core information of the Figure, not additional information added to explain or qualify. At most, the allelic imbalance, retention of heterozygosity, and microsatellite instability data of Figure 2 could be interpreted to be the arbitrary gene- or protein-related data recited in the claim, and could not also be the annotations that are required to be displayed alongside that data. Hence, there are additional grounds for allowing claim 22 and the claims dependent therefrom.

Claim 23 depends from claim 22 and additionally requires that the annotations be gene ontology annotations. Gene ontology annotations are strictly defined, standardized terms that describe attributes of genes – see, for example, http://wiki.geneontology.org/index.php/GO_FAQ#What_is_GO.3F for an explanation of the Gene Ontology project that addresses the need for consistent descriptions of gene products in different databases, and includes a discussion of gene ontology annotations. Figure 2 of Partridge, cited by the Examiner as teaching gene ontology annotations, does not include any such terms. Hence, there are additional grounds for allowing claim 23.

Claim 24 depends from claim 1 through claim 21 and additionally requires that the additional information displayed alongside the display of the arbitrary gene- or protein-related data be selected from the group consisting of CGH data, protein levels, relevance scores and relevance densities. The Examiner points to Figure 2 of Partridge, identifying "allelic imbalance, retention of heterozygosity, and microsatellite instability" as relevance scores. The specification of the current invention (paragraphs 0093-0094) defines the relevance score or p-value as the separation value of the particular genes being analyzed, indicating how well they can separate tumors from normals based on expression values. None of the data to which the Examiner points are relevance scores. Hence, there are additional grounds for allowing claim 24.

Claim 26 depends from claim 1 through claim 21 and additionally requires that the arbitrary gene- or protein-related data be displayed in scatter plot format. The Examiner states "Figure 2 of Partridge et al. is interpreted to be a scatter plot". Applicant respectfully submits that the matrices shown in Figure 2 cannot be scatter plots. A scatter plot displays data that can be characterized by pairs of first and second numeric values as a simple collection of points, where the horizontal position of each point is determined by the corresponding first numeric value and the vertical position is determined by the corresponding second numeric value. No such data and no such plot is shown anywhere in Partridge. Hence, there are additional grounds for allowing claim 26.

Claim 30 depends from claim 18 and additionally requires that row vectors of the

values in the rows of the matrix be calculated, and that an auxiliary process be used to obtain cluster data for said row vectors; said cluster data being displayed along side said display of said arbitrary gene- or protein-related data. The Examiner points to Figure 2 of Partridge as providing the required teachings, appearing to identify the data in the rows as row vectors, and identifying the vertical black bars as displaying cluster data. First, the cited figure does include rows of cells containing data, but there is no teaching regarding the calculation of any row vectors. Second, at most the "clusters" indicated by the bars are clusters corresponding to rows, not to row vectors. Hence, there are additional grounds for allowing claim 30 and the claims dependent therefrom.

Claim 33 depends from claim 30 and additionally requires that the cluster data is displayed in a multi-column matrix. The black bars identified by the Examiner as the recited cluster data are at most a single column matrix. The Examiner offers an alternative interpretation of the recited cluster data as the data inside the matrices, but Applicant respectfully submits that the latter data is not displayed **along side** the gene- or protein-related data of the matrices, and hence, cannot be taken to be the recited cluster data. Accordingly, there are additional grounds for allowing claim 33.

Claim 34 depends from claim 1 and additionally requires that a portion of the total number of columns be associated with experiments taken from normal, healthy tissue, and another portion of the total number of columns be associated with experiments taken from tissue exhibiting an abnormality, said method further comprising dividing the matrix into two smaller matrices with a first matrix containing the columns associated with normal experiments and a second matrix containing the columns associated with abnormal experiments, and wherein said matching and displaying are performed with regard to both first and second matrices. The Examiner points to the top set of matrices in Figure 2 of Partridge as the recited second matrix and the bottom matrix as the recited first matrix.

In both the claim and Partridge, the columns correspond to experiments. However, in Partridge, the two matrices do not result from a division according to columns associated with normal and abnormal experiments respectively. At most, they result from a division according to **rows** (markers) associated with normal and abnormal chromosomal loci. Hence, there are additional grounds for allowing claim 34 and the claims dependent therefrom.

Claim 36 depends from claim 34 and additionally requires that a relevance score be calculated for at least one row of the matrices by comparing expression values in the first matrix with expression values in the second matrix, and displaying at least one calculated relevance score along side the row to which each pertains. The Examiner identifies the contents of the four rightmost columns of the matrices in Figure 2 of Partridge as relevance scores. As noted above with respect to claim 24, the specification of the current invention (paragraphs 0093-0094) defines the relevance score or p-value as the separation value of the particular genes being analyzed, indicating how well they can separate tumors from normals based on expression values. None of the data to which the Examiner points are relevance scores as so defined. Hence, there are additional grounds for allowing claim 36 and the claims dependent therefrom.

Claim 37 depends from claim 36 and additionally requires that said calculating is interactively initiated via a user interface. The Examiner states "Figure 2 on page 320 of Partridge et al. is interpreted to be the user interface". Applicant submits that even if one were motivated to generate a static display such as Figure 2, there is no teaching of any action being initiated by such user "interaction" let alone the calculating recited in the claim. Accordingly, there are additional grounds for allowing claim 37.

Claim 55 depends from claim 1 and further requires that additional information related to one or more genes characterized by said arbitrary gene- or protein-related data be selected and displayed along side of said display of the arbitrary gene- or protein-related data and positioned relative to the respective locations on the chromosome map of the respective genes characterized by said arbitrary gene- or protein-related data. The Examiner points to Figure 2 of Partridge, identifying the "additional information of candidate tumor gene suppressor regions" as the additional information recited in the claim. The cited information is positioned relative to the matrices of Partridge, which the Examiner identifies as containing the recited gene- or protein-related data but there is no teaching of any positioning relative to the chromosome maps which are shown only in Figure 1. Hence, there are additional grounds for allowing claim 55 and the claims dependent therefrom.

Claim 56 depends from claim 55 and additionally specifies that the additional information comprise at least one of **polymorphism measurements, annotations, transcription factor binding sites, RNA expression values, allele information, alternative exon splicing data, mapping of CGH gene amplification/deletions, and protein abundance**. The Examiner states that "annotations in Figure 2 of Partridge" satisfy this requirement. At most, the "allelic imbalance" data in Figure 2 could be interpreted to be allele information, but these data are included as elements of the matrices which the Examiner interprets to be included as the gene- or protein-related data. They cannot also be taken to be information additional to the gene- or protein-related data, Applicant finds no teaching of any of the other types of recited information anywhere in Figure 2. Hence, there are additional grounds for allowing claim 56.

Claim 81 depends from claim 80 and further requires that the first and second matrices be displayed **in color-coding** as heat maps. The Examiner points to the matrices of Figure 2 of Partridge as satisfying this requirement. At most, the cited matrices represent cell values by various types of shading or patterning. Applicant finds no teaching in Partridge regarding any color coding. Hence, there are additional grounds for allowing claim 81.

Claim 82 depends from claim 80 and additionally requires that a relevance score for at least one row of the matrices be calculated by comparing expression values in the first matrix with expression values in the second matrix, and be displayed along side the row to which it pertains. First, as noted above with respect to claim 24, none of the data to which the Examiner points are relevance scores, as defined in the specification of the current invention. Second, the Examiner states that those data are "comparable between the bottom matrix of controls and the row of interest in the top three matrices". This is not equivalent to teaching that those data are **calculated by** such comparing. Furthermore, the **results** of such comparing are not displayed alongside the rows. Accordingly, there are additional grounds for allowing claim 82 and the claims dependent therefrom.

Claim 83 depends from claim 82 and has an additional limitation corresponding to that of claim 37. Applicant submits that there are the same additional grounds for allowing claim 82 as in the case of claim 37.

The Examiner rejected claims 5, 6, 8, 9, and 11 under 35 U.S.C. 103(a) as being unpatentable over Partridge et al. in view of Reeves as applied to claims 1-4, 7, 10, 12-37, 40, 55, 56, 80-83, and 86 above in further view of Koleszar et al. [US Patent 6,519,583; issued 11 February 2003; filed 27 July 1999]. Applicant submits that as currently amended, claims 5, 6, 8, 9, and 11 are not obvious in view of the cited prior art.

The Examiner states that the combination of Partridge and Reeves teaches the limitations of claims 5-6, 8, 9 and 11, except for the limitations requiring particular display features. The Examiner looks to Koleszar, whose teachings are directed towards the graphical display of computer-based biomolecular sequence information for the missing teachings. The Examiner maintains that it would have been obvious to apply the display features taught by Koleszar to the method of Partridge/Reeves to display "the genomic data in a more convenient and user-friendly format [see, for example, column 2, lines 5-9 of Koleszar]".

As noted above with respect to claim 1, from which claims 5, 6, 8, 9, and 11 depend, the combination of Partridge and Reeves does not teach the base claim limitation requiring that the gene- or protein- related data that are imported and then displayed in adjacent positions on a chromosome map where the data identifiers match the predetermined chromosome map identifiers include data **other than markers or identifiers** specifying genetic loci of that gene- or protein-related data on the chromosome maps. Koleszar does not provide the missing teachings. Accordingly, Applicant submits that as currently amended, claims 5, 6, 8, 9, and 11 are not obvious in view of the cited prior art.

With respect to claim 6, consider the additional requirement that **information on the display that a user is not interested in viewing be queried and cut**. The Examiner points to the Abstract and Figure 2A of Koleszar as providing this teaching. Applicant finds no teaching in the cited passage or figure regarding querying and cutting as specified. At most, the figure shows that the displayed view may be zoomed out as well as in, so that information on the display that a user is less interested in viewing may be shown at lower magnification, but this is not equivalent to cutting that information. Hence, there are additional grounds for

allowing claim 6.

Claim 8, which depends from claim 1 through claim 7, has been amended to require that a high level view of all of said chromosome maps and gene- or protein-related data, a mid-level view displaying a magnified view of a selected portion of said high level view, and a detailed view displaying expanded, detailed information characterizing a selected portion of said mid-level view be simultaneously displayed. At most, Figure 4A of Koleszar shows two views of chromosome maps at different magnifications, not three, and shows only one view of related data. Hence, there are additional grounds for allowing claim 8 and the claims dependent therefrom.

With respect to claim 9, which depends from claim 8, Applicant finds no teaching in Figure 4a or elsewhere that said high-level view, mid-level view and detailed view all be **interlinked** so that **changing one view automatically changes the other two views** in the same way, substantially simultaneously. Applicant finds no such teaching in Figure 4A or elsewhere in Koleszar. Hence, there are additional grounds for allowing claim 9.

With respect to claim 11, Applicant finds no teaching of any popup dialogs to display additional details relative to a selected portion of the display. The Examiner points to "pop-up buttons" in Figure 4A of Koleszar as providing this teaching. But Applicant finds no teaching that activation of any of the cited buttons results in the display of additional details relative to a selected portion of the display. Hence, there are additional grounds for allowing claim 11.

The Examiner rejected claims 38, 43, 84, and 89 under 35 U.S.C. 103(a) as being unpatentable over Partridge et al. in view of Reeves as applied to claims 1-4, 7, 10, 1237, 40, 55, 56, 80-83, and 86 above, and further in view of McCully [US Patent 4,383,994 issued 17 May 1983; filed 19 January 1982]. Applicant submits that as currently amended, claims 38, 43, 84, and 89 are not obvious in view of the cited prior art.

The Examiner states that the combination of Partridge and Reeves teaches all the limitations of claims 38 and 84 except for the use of p values. The Examiner looks to McCully for the missing teachings. The Examiner maintains that it would have been obvious

to apply the p-value teachings of McCully to analyze the arrays of Partridge to provide "improved and more advanced statistical analysis".

First, as noted above with respect to claims 36 and 82, from which claims 38 and 84 respectively depend, the combination of Partridge and Reeves fails to teach the limitations regarding data other than markers or identifiers, or relevance scores, or matrix division according to columns corresponding to normal and abnormal measurements. McCully does not provide the missing teachings.

Second, McCully teaches the use of a p-value as a statistical cut-off for determining the deviation between the control and the experimental sample. The Examiner has not pointed to any teaching as to how one would modify Partridge to utilize the p-values of McCully. Accordingly, Applicant submits that claims 38 and 84 are not obvious in view of the cited prior art.

The Examiner states that the combination of Partridge and Reeves teaches all the limitations of claims 43 and 89 except for requiring that the relevance scores be filtered by setting at least one relevance score limit value and displaying only those relevance scores which are greater than or equal to at least one relevance score limit value. The Examiner points to McCully for the additional teaching, stating that the "p value acts as a statistical cut off for determining deviation between a control and experimental sample".

First, as noted with respect to claims 36 and 82, from which claims 43 and 89 depend, the combination of Partridge and Reeves fails to teach the limitations regarding data other than markers or identifiers, or relevance scores, or matrix division according to columns corresponding to normal and abnormal measurements. McCully does not provide the missing teachings. Second, the statement that a p-value (relevance score) itself may act as a statistical cut off is not equivalent to asserting that relevance scores are filtered by setting a limit value and displaying only those relevance scores which are greater than or equal to that value, as the claim requires. Accordingly, Applicant submits that claims 43 and 89 are not obvious in view of the cited prior art.

The Examiner rejected claims 39, 42, 85 and 88 under 35 U.S.C. 103(a) as being unpatentable over Partridge et al. in view of Reeves as applied to claims 1-4, 7, 10, 1237, 40, 55, 56, 80-83, and 86 above, and further in view of Ben-Dor et al. [Genome Research, 2000, volume 10, pages 365-378]. Applicant submits that as currently amended, claims 39, 42, 85 and 88 are not obvious in view of the cited prior art.

The Examiner states that the combination of Partridge and Reeves teaches all the limitations of claims 39, 42, 85 and 88 except for those concerning **line maps** or **relevance density scores.** The Examiner looks to Ben-Dor for the missing teachings. The Examiner maintains that it would have been obvious to apply the teachings of Ben-Dor to the method of Partridge/Reeves as "an alternate means of analyzing the mappings of chromosomes".

First, as noted above with respect to claims 36 and 82, from which claims 39, 42, 85 and 88 respectively depend, the combination of Partridge and Reeves fails to teach the limitations regarding data other than markers or identifiers, or relevance scores, or matrix division according to columns corresponding to normal and abnormal measurements. Ben-Dor does not provide the missing teachings.

Second, the Examiner has not suggested any benefit that would be gained by the method of Partridge/Reeves in applying the "alternate means" of Ben-Dor. There are a very large number of possible alternate means of analyzing chromosome mapping, and no obvious reason why the means of Ben-Dor would confer a particular advantage to Partridge/Reeves absent the present application as a guide. Accordingly, Applicant submits that claims 39, 42, 85 and 88 are not obvious in view of the cited prior art.

Claims 39 and 85 also require that a relevance score be calculated and displayed. The Examiner points to Figure 7 of Ben-Dor, but Applicant finds no teaching in the cited figure or accompanying text regarding any relevance score as defined in the current invention. Hence, there are additional grounds for allowing claims 39 and 85.

Claims 42 and 88 require that a **relevance density score** based upon distances between genetic locations and relevance scores **be defined**, and chromosomal **locations containing relevance density scores greater than or equal to** the defined relevance density

score be identified. The Examiner points to Figure 6 of Ben-Dor for these teachings, stating that the line maps indicate "scores and distances between the relevant markers". Applicant finds no teaching in the cited figure or associated text of the definition of any relevance density score or of the identification of chromosomal locations based on the values of relevance density scores relative to that defined relevance density score. At most, the figure indicates that distances may be defined between marked genetic locations. Hence, there are additional grounds for allowing claims 42 and 88.

The Examiner rejected claims 41 and 87 under 35 U.S.C. 103(a) as being unpatentable over Partridge et al. in view of Reeves as applied to claims 1-4, 7, 10, 12-37, 40, 55, 56, 80-83, and 86 above, and further in view of Bodzin et al. [US PGPUB 2003/0139886 Al published 24 July 2003; filed 5 September 2002] Applicant submits that as currently amended, claims 41 and 87 are not obvious in view of the cited prior art.

The Examiner states that the combination of Partridge and Reeves teaches all the limitations of claims 41 and 87 except for the calculation and display of scores in a binary code. The Examiner looks to Bodzin for the missing teachings. The Examiner maintains that it would have been obvious to apply the teachings of Bodzin to the method of Partridge/Reeves as "a convenient means of normalization of the instant set of data [see paragraph 0037 and Figure 15 of Bodzin et al.]".

First, as noted above with respect to claims 36 and 82, from which claims 41 and 87 respectively depend, the combination of Partridge and Reeves fails to teach the limitations regarding data other than markers or identifiers, or relevance scores, or matrix division according to columns corresponding to normal and abnormal measurements. Bodzin does not provide the missing teachings.

Second, Applicant disagrees with the Examiner's reading of the cited passages. The cited paragraph in Bodzin teaches that existing normalization methods that use controls are imperfect, and the cited figure in Bodzin is a calibration slide, but neither teaches the calculation and display of relevance scores in a binary code, as the claims require.

Accordingly, Applicant submits that claims 41 and 87 are not obvious in view of the cited prior art.

The Examiner rejected claims 44, 46-47, 90 and 92-93 under 35 U.S.C. 103(a) as being unpatentable over Partridge et al. in view of Reeves as applied to claims 1-4, 7, 10, 1237, 40, 55, 56, 80-83, and 86 above, and further in view of Pollack et al. [Nature Genetics, volume 23, 1999, pages 41-46]. Applicant submits that as currently amended, claims 44, 46-47, 90 and 92-93 are not obvious in view of the cited prior art.

The Examiner states that the combination of Partridge and Reeves teaches all the limitations of claims 44, 46-47, 90 and 92-93 except those relating to chromosomal copy abnormality data, or the interlacing and display of chromosomal copy number information. The Examiner looks to Pollack for the missing teachings. The Examiner maintains that it would have been obvious to apply the teachings of Pollack to those of Partridge/Reeves to "allow more conveniently acquired and well resolved data [see lines 13-17 of abstract on page 41 and Figure 5a of Pollack et al.]"

As noted above with respect to claims 34 and 80, from which claims 44, 46-47, 90 and 92-93 respectively depend, the combination of Partridge and Reeves fails to teach the limitations regarding data other than markers or identifiers, or matrix division according to columns corresponding to normal and abnormal measurements. Pollack does not provide the missing teachings. Accordingly, Applicant submits that claims 44, 46-47, 90 and 92-93 are not obvious in view of the cited prior art.

Claims 46 and 92 also require that the chromosomal copy number abnormality data be **provided in columns interlaced with the columns of expression data in the first and second matrices.** The Examiner points to Figure 5a of Pollack as providing this teaching, but the cited figure at most shows two side-by-side matrices, one of copy number data and one of expression data. No columns of one type are interlaced with columns of the other type. Hence, there are additional grounds for allowing claims 46 and 92.

The Examiner rejected claims 48 and 94 under 35 U.S.C. 103(a) as being

unpatentable over Partridge et al. in view of Reeves in view of Pollack et al. as applied to claims 1-4, 7, 10, 12-37, 40, 44, 46-47, 55, 56, 80-83, 86, 90 and 92-93 above, and further in view of Ben-Dor et al. Applicant submits that as currently amended, claims 48 and 94 are not obvious in view of the cited prior art.

The Examiner states that the combination of Partridge and Reeves teaches all the limitations of claims 48 and 94 except those relating to the use of line maps. The Examiner points to Ben-Dor for the missing teachings. The Examiner maintains that it would have been obvious to apply the teachings of Ben-Dor to those of Partridge/Reeves as "an alternate means of analyzing the mappings of chromosomes".

As noted above with respect to claims 44 and 90, from which claims 48 and 94 respectively depend, the combination of Partridge and Reeves fails to teach the limitations regarding data other than markers or identifiers, or matrix division according to columns corresponding to normal and abnormal measurements. Ben-Dor does not provide the missing teachings. In addition, the Examiner has not pointed to any advantage in using this alternate means of analyzing the mappings over any of the other possible alternate means in the prior art, absence the present application as a guide. Accordingly, Applicant submits that claims 48 and 94 are not obvious in view of the cited prior art.

Applicant notes the Examiner's statement that claims 45, 49-54, and 95-101 are free of the prior art. Applicant submits that the above-amendments overcome any rejections based on 35 U.S.C. 101 and rejections based on the above-discussed grammatical informalities. Accordingly, Applicant submits that these claims are now in condition for allowance. These claims will be placed in independent form if necessary when prosecution of this application on the merits is closed.

Respectfully Submitted,

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